ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09534,8618
ATTN: NEW RULES CASES	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
· · · · · ·	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
"bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
— —	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



TAIR: NIVITA 53

1600

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TIME: 10:46:58 > Non on P. 5
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             Ebskamp, Michael
      4
             Geerts, Hendrikis
             Weisbeek, Petrus
      4 <126 - TITLE OF INVENTION: Production of Oligosaccharides in Transpenic Plants
     10 <130 - FILE REFERENCE: ARNO-1-15313
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     46 Gly Lys Frc Fro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
     47 5
                            10
    49 god gåd ggt aag ogg ach ggd tgh atg agg tgg the gog tgt god ach
     50 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
     53 pig ong acq goo nog goo ang goy yig gng gig gio goo yeo acq one
     54 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Gly Ala Thr Leu
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RAW SEQUENCE LISTING

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73 ggc ása gás tag gás gas	quo ata qaa tag qoo	cae deo gig tub saa	441
74 Gly Thr Asp Trp Asp Asp			
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79 135	140	145	
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82 Trp Tyr Asp Ile Leu Gly			
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86 Asn Gly Thr Val Ile Met			
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95 200	205	210	
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99 215 101 gac gag tcc gac gag aca 102 Asp Glu Ser Asp Glu Thr 103 230 105 cac gac ggc cac cac gac 106 His Asp Gly His His Asp 107 245 250 109 ttc ctc aac tac gag ctc 110 Fhe Leu Asr. Tyr Glu Let 111 265 113 acc ggc gág tgg gag tgc	220 tgg sgc acc ctc ctc Trp Arg Thr Leu Lei ggc atc gcc atg atc Gly Ile Ala Met Mer atc ccg ggc atc ttc Ile Pro Gly Ile Lei 270 atc gac ttc tac ccc	225 c ggg too aag gas gas u Gly Ser Lys Asp Asp 240 g tac aag acc aag gas t Tyr Lys Thr Lys Asp 5 260 g cac egg gtg gtg egs u His Arg Val Val Arg 275 c gtc gge egg aga ags	
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						Leu				Arg	Thr		Fro	€	Ala	Met.	
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271	Thr		Trp	Tyr	Asp	Glu		Asp	Glu	Thr	Trp		Thr	1.64	Leu	Gly	
272	225					236					235					240	
275		Lys	Ašp	Asp	His	Asp	Gly	$\mathrm{H}^{2}\mathcal{S}$	His	Asp	Gly	1:e	Ala	Mest	Met		
276					245					250					255		
	Lys	Thr	Lys	Asp	$F \vdash_{i} \in$	Leu	Asn	Tyr	Glu	Leu	11e	Pro	Gly	${\tt Ile}$	Leu	Hls	
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	ĀΩĢ			Arg	Try	7 y	314	Tri	71.12	37.0	di	ASE		771	Fro	7.11	
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1ATE: 1 11 2 -RAW SEQUENCE LISTING TIME: 1 :4::5: HATENT APPLICATION: US/09/534,861B Insur Not : A:\15313SEQrev.txt output N:\CRF4\01172003\I534861B.raw 1-7 Mly Ara Ara Ser Ser Asp Ash Ser ton 31d Met Led Bis Val Led Lys 2.145 191 Ala Cor Mc Asp Asp Sid Arr His Asp Tyr Tyr Jer led tly The Tyr 196 Asp Jor Ala Ala Ash Thr Trp Thr Fro Ille Asp Fr. Old Ied Asp Ied 325 299 Gly Ile Gly Let Arg Tyr Asp Trp Gly Lys Fhe Tyr Ala Ser Thr Ser 345 Fhe Tyr Asp Fro Ala Lys Ash Arg Arg Val Leu Met Gly Tyr Val Gly 360 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser lle 311 Gln Ser Val Fro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn 395 390 315 Leu Leu leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Ass Ala 405 410 415 31) Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile 420 425 Pro Leu Arg Gin Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His 435 440 445 327 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr 455 460 331 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Fro 470 475 33b Fhe Gly Leu Leu Vâl Leu Ala Ala Gly Asp Arg Arg Gly Glu Gir Thr 490 485 339 Ala Val Tyr Fhe Tyr Val Ser Arg Sly Leu Asp Gly Gly Leu His Thr 505 5.00 510 34) Ser Phe Cys Glm Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr 520 34% Lys Arg Val lie Gly Ser Thr Val Fro Val Leu Asp Gly Giu Ala Leu 535 540 351 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Fhe Asp Met 550 555 355 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr 565 570 359 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val 590 585 590 363 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln 600

item 10

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in Leu Ser Ash Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser

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375 <2100 SEQ ID NO: 3

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376 <211> LENGTH: 30 370 -2125 TYFE: MMA 🚐

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RAW SEQUENCE LISTING ERROR SUMMARY FATERITY AFERITATION: US/09/534,861B

light det : A:\15313SEQrev.txt

N:\CRF4\01172003\I534861B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seg#:11; Maa Fos. 6,12,15 Seg#:12; Maa Fos. 5,7,4,11,13

VERIFICATION SUMMARY

HATENT APPLICATION: US/09/534,861B

light 300 : A:\15313SEQrev.txt

arrat 39-t: N:\CRF4\01172003\I534861B.raw

Li12 Mi. 71 Or Current Application Number guiffers, Replaced Current Application Number
Li471 Mi.41 Wi 4+ "n" or "Maa" used, ior SF. ID=:11 arrent s.:
Li4+7 Mi.41 Wi 4+ "n" or "Maa" used, ior SE, ID=:12 arrent s.: